

SEQUENCE LISTING

<110> Sheppard, Paul O.
Jaspers, Stephen R.

<120> CONNECTIVE TISSUE GROWTH FACTOR HOMOLOGS

<130> 97-75

<150> US 60/075,300

<151> 1998-02-20

<160> 34

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1142

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (17)...(1078)

<400> 1

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ggc ctg gca cag ttc tgc tgc agg gta cag ggc act gga cca tta gat	100
Gly Leu Ala Gln Phe Cys Cys Arg Val Gln Gly Thr Gly Pro Leu Asp	
15 20 25	
aca aca cct gaa gga agg cct gga gaa gtg tca gat gca cct cag cgt	148
Thr Thr Pro Glu Gly Arg Pro Gly Glu Val Ser Asp Ala Pro Gln Arg	
30 35 40	
aaa cag ttt tgt cac tgg ccc tgc aaa tgc cct cag cag aag ccc cgt	196
Lys Gln Phe Cys His Trp Pro Cys Lys Cys Pro Gln Gln Lys Pro Arg	
45 50 55 60	
tgc cct cct gga gtg agc ctg gtg aga gat ggc tgt gga tgc tgt aaa	244
Cys Pro Pro Gly Val Ser Leu Val Arg Asp Gly Cys Gly Cys Cys Lys	
65 70 75	

atc tgt gcc aag caa cca ggg gaa atc tgc aat gaa gct gac ctc tgt	292
Ile Cys Ala Lys Gln Pro Gly Glu Ile Cys Asn Glu Ala Asp Leu Cys	
80 85 90	
gac cca cac aaa ggg ctg tat tgt gac tac tca gta gac agg cct agg	340
Asp Pro His Lys Gly Leu Tyr Cys Asp Tyr Ser Val Asp Arg Pro Arg	
95 100 105	
tac gag act gga gtg tgt gca tac ctt gta gct gtt ggg tgc gag ttc	388
Tyr Glu Thr Gly Val Cys Ala Tyr Leu Val Ala Val Gly Cys Glu Phe	
110 115 120	
aac cag gta cat tat cat aat ggc caa gtg ttt cag ccc aac ccc ttg	436
Asn Gln Val His Tyr His Asn Gly Gln Val Phe Gln Pro Asn Pro Leu	
125 130 135 140	
ttc agc tgc ctc tgt gtg agt ggg gcc att gga tgc aca cct ctg ttc	484
Phe Ser Cys Leu Cys Val Ser Gly Ala Ile Gly Cys Thr Pro Leu Phe	
145 150 155	
ata cca aag ctg gct ggc agt cac tgc tct gga gct aaa ggt gga aag	532
Ile Pro Lys Leu Ala Gly Ser His Cys Ser Gly Ala Lys Gly Gly Lys	
160 165 170	
aag tct gat cag tca aac tgt agc ctg gaa cca tta cta cag cag ctt	580
Lys Ser Asp Gln Ser Asn Cys Ser Leu Glu Pro Leu Leu Gln Gln Leu	
175 180 185	
tca aca agc tac aaa aca atg cca gct tat aga aat ctc cca ctt att	628
Ser Thr Ser Tyr Lys Thr Met Pro Ala Tyr Arg Asn Leu Pro Leu Ile	
190 195 200	
tgg aaa aaa aaa tgt ctt gtg caa gca aca aaa tgg act ccc tgc tcc	676
Trp Lys Lys Lys Cys Leu Val Gln Ala Thr Lys Trp Thr Pro Cys Ser	
205 210 215 220	
aga aca tgt ggg atg gga ata tct aac agg gtg acc aat gaa aac agc	724
Arg Thr Cys Gly Met Gly Ile Ser Asn Arg Val Thr Asn Glu Asn Ser	
225 230 235	

100115551109671

aac tgt gaa atg aga aaa gag aaa aga ctg tgt tac att cag cct tgc 772
 Asn Cys Glu Met Arg Lys Glu Lys Arg Leu Cys Tyr Ile Gln Pro Cys
 240 245 250

gac agc aat ata tta aag aca ata aag att ccc aaa gga aaa aca tgc 820
 Asp Ser Asn Ile Leu Lys Thr Ile Lys Ile Pro Lys Gly Lys Thr Cys
 255 260 265

caa cct act ttc caa ctc tcc aaa gct gaa aaa ttt gtc ttt tct gga 868
 Gln Pro Thr Phe Gln Leu Ser Lys Ala Glu Lys Phe Val Phe Ser Gly
 270 275 280

tgc tca agt act cag agt tac aaa ccc act ttt tgt gga ata tgc ttg 916
 Cys Ser Ser Thr Gln Ser Tyr Lys Pro Thr Phe Cys Gly Ile Cys Leu
 285 290 295 300

gat aag aga tgc tgt atc cct aat aag tct aaa atg att act att caa 964
 Asp Lys Arg Cys Cys Ile Pro Asn Lys Ser Lys Met Ile Thr Ile Gln
 305 310 315

ttt gat tgc cca aat gag ggg tca ttt aaa tgg aag atg ctg tgg att 1012
 Phe Asp Cys Pro Asn Glu Gly Ser Phe Lys Trp Lys Met Leu Trp Ile
 320 325 330

aca tct tgt gtg tgt cag aga aac tgc aga gaa cct gga gat ata ttt 1060
 Thr Ser Cys Val Cys Gln Arg Asn Cys Arg Glu Pro Gly Asp Ile Phe
 335 340 345

tct gag ctc aag att ctg taaaaccaag caaatggggg aaaagttagt 1108
 Ser Glu Leu Lys Ile Leu
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caatcctgtc atataataaa aaaattagtg agta 1142

<210> 2

<211> 354

<212> PRT

<213> Homo sapiens

<400> 2

Met Gln Gly Leu Leu Phe Pro Thr Leu Leu Leu Ala Gly Leu Ala Gln
 1 5 10 15
 Phe Cys Cys Arg Val Gln Gly Thr Gly Pro Leu Asp Thr Thr Pro Glu
 20 25 30

Gly Arg Pro Gly Glu Val Ser Asp Ala Pro Gln Arg Lys Gln Phe Cys
 35 40 45
 His Trp Pro Cys Lys Cys Pro Gln Gln Lys Pro Arg Cys Pro Pro Gly
 50 55 60
 Val Ser Leu Val Arg Asp Gly Cys Gly Cys Cys Lys Ile Cys Ala Lys
 65 70 75 80
 Gln Pro Gly Glu Ile Cys Asn Glu Ala Asp Leu Cys Asp Pro His Lys
 85 90 95
 Gly Leu Tyr Cys Asp Tyr Ser Val Asp Arg Pro Arg Tyr Glu Thr Gly
 100 105 110
 Val Cys Ala Tyr Leu Val Ala Val Gly Cys Glu Phe Asn Gln Val His
 115 120 125
 Tyr His Asn Gly Gln Val Phe Gln Pro Asn Pro Leu Phe Ser Cys Leu
 130 135 140
 Cys Val Ser Gly Ala Ile Gly Cys Thr Pro Leu Phe Ile Pro Lys Leu
 145 150 155 160
 Ala Gly Ser His Cys Ser Gly Ala Lys Gly Gly Lys Lys Ser Asp Gln
 165 170 175
 Ser Asn Cys Ser Leu Glu Pro Leu Leu Gln Gln Leu Ser Thr Ser Tyr
 180 185 190
 Lys Thr Met Pro Ala Tyr Arg Asn Leu Pro Leu Ile Trp Lys Lys Lys
 195 200 205
 Cys Leu Val Gln Ala Thr Lys Trp Thr Pro Cys Ser Arg Thr Cys Gly
 210 215 220
 Met Gly Ile Ser Asn Arg Val Thr Asn Glu Asn Ser Asn Cys Glu Met
 225 230 235 240
 Arg Lys Glu Lys Arg Leu Cys Tyr Ile Gln Pro Cys Asp Ser Asn Ile
 245 250 255
 Leu Lys Thr Ile Lys Ile Pro Lys Gly Lys Thr Cys Gln Pro Thr Phe
 260 265 270
 Gln Leu Ser Lys Ala Glu Lys Phe Val Phe Ser Gly Cys Ser Ser Thr
 275 280 285
 Gln Ser Tyr Lys Pro Thr Phe Cys Gly Ile Cys Leu Asp Lys Arg Cys
 290 295 300
 Cys Ile Pro Asn Lys Ser Lys Met Ile Thr Ile Gln Phe Asp Cys Pro
 305 310 315 320
 Asn Glu Gly Ser Phe Lys Trp Lys Met Leu Trp Ile Thr Ser Cys Val
 325 330 335
 Cys Gln Arg Asn Cys Arg Glu Pro Gly Asp Ile Phe Ser Glu Leu Lys
 340 345 350
 Ile Leu

<210> 3

<211> 1062

<212> DNA
<213> Artificial Sequence

<220>
<223> Degenerate sequence

<221> misc_feature
<222> (1)...(1062)
<223> n = A,T,C or G

<400> 3

atgcarggny tnynttlycc nacnytnytn ytngcnggny tngcncartt ytgytgymgn	60
gtncarggna cnggncnny ngayacnacn ccngarggnm gncnggnga rgtnwsngay	120
gcncncarm gnaarcartt ytgycaytg ccntgyaart gyccncarca raarccnmgn	180
tgycncncng gngtnwsnyt ngtnmgngay ggntgyggnt gytgyaarat htgygcnaar	240
carcnggng arathtgayaa ygargcngay ytnthygagc cncayaargg nyntaytg	300
gaytaywsng tngaymgncc nmgtaygar acngngntnt gygcntayyt ngtngcngtn	360
ggntgygart tyaycargt ncaytaycay aayggncarg tnttycarcc naayccnytn	420
ttywsntgyy tntgygtws ngngcncath ggntgyacnc cnynttyat hccnaarytn	480
gcnggnwsnc aytgywsng ngcnaarggn ggnaaraarw sngaycarws naaytgysn	540
ytngarccny tnytnarca rytwnsnacn wsntayaara cnatgccngc ntaymgnay	600
ytncnytna thtgaaraa raartgytn gtncargcna cnaartggac nccntgywsn	660
mgnacntgyg gnatgggnat hwsnaaymgn gtnacnaayg araaywsnaa ytgygaratg	720
mgnaargara armgnyntng ytayathcar ccntgygayw snaayathyt naaracnath	780
aarathccna arggnaarac ntgycarccn acnttycary tnwsnaargc ngaraartty	840
gtnttywsng gntgywsnws nacncarwsn tayaarccna cnttytgygg nathtgytn	900
gayaarmgnt gytgyathcc naayaarwsn aaratgatha cnathcartt ygaytgyccn	960
aaygarggnw snttyaartg gaaratgytn tggathacnw sntgygtntg ycarmgnaay	1020
tgymngarc cngngngayt httywsngar ytnaarathy tn	1062

<210> 4
<211> 279
<212> DNA
<213> Mus musculus

<400> 4

atccccagag gagaaacatg tcaaccact ttccaactcc ccaaagctga aaaatttgtt	60
ttttctggat gctcaagcac tcagagttac agaccactt tctgtggaat atgcctggac	120
aagagatgct gtgtcccaa caaatctaaa atgattactg ttaggtttga ctgccccagt	180
gaagggtcat ttaagtggca gatgctgtg gtcacatctt gtgtgtgtca gagggactgc	240
agagaaccag gagatatatt ttctgagctc aggattcta	279

<210> 5
<211> 93
<212> PRT

10011559.11501

<213> Mus musculus

<400> 5

Ile	Pro	Arg	Gly	Glu	Thr	Cys	Gln	Pro	Thr	Phe	Gln	Leu	Pro	Lys	Ala
1				5				10					15		
Glu	Lys	Phe	Val	Phe	Ser	Gly	Cys	Ser	Ser	Thr	Gln	Ser	Tyr	Arg	Pro
			20				25					30			
Thr	Phe	Cys	Gly	Ile	Cys	Leu	Asp	Lys	Arg	Cys	Cys	Val	Pro	Asn	Lys
		35				40					45				
Ser	Lys	Met	Ile	Thr	Val	Arg	Phe	Asp	Cys	Pro	Ser	Glu	Gly	Ser	Phe
	50				55				60						
Lys	Trp	Gln	Met	Leu	Trp	Val	Thr	Ser	Cys	Val	Cys	Gln	Arg	Asp	Cys
65				70				75					80		
Arg	Glu	Pro	Gly	Asp	Ile	Phe	Ser	Glu	Leu	Arg	Ile	Leu			
			85					90							

<210> 6

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer ZC14882

<400> 6

aacttttccc ccatttgctt gg

22

<210> 7

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer ZC14883

<400> 7

acaaaatgga ctccctgctc c

21

<210> 8

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer ZC15909

10011660-10601

<400> 8
 tcgtccaacg actataaaga gg 22

 <210> 9
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> oligonucleotide primer ZC14885

 <400> 9
 ttgctgtcgc aaggctgaat g 21

 <210> 10
 <211> 21
 <212> DNA
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 <220>
 <223> oligonucleotide primer ZC15911

 <400> 10
 aggctgtcct ctaagcgta c 21

 <210> 11
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 <212> DNA
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 <220>
 <223> oligonucleotide primer ZC14884

 <400> 11
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 <210> 12
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 <223> oligonucleotide primer ZC15910

<400> 12
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 <210> 14
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 <220>
 <223> oligonucleotide primer ZC15089

 <400> 14
 tccctaataa gtctaaaa 18

 <210> 15
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> oligonucleotide primer ZC15092

 <400> 15
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 <210> 16
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 <213> Artificial Sequence

 <220>
 <223> Peptide tag

 <400> 16

<220>
<223> oligonucleotide primer ZC16422

<210> 18
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<220>
<223> oligonucleotide primer ZC16421
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<210> 20
<211> 30
<212> DNA
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<220>
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<400> 20

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30

<210> 21

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer ZC16423

<400> 21

accctcgaga tgcaggggct.cctcttcccc

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<210> 22

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer ZC16409

<400> 22

ccgggatccc agaatcttga gctcagaaaa

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<210> 23

<211> 127

<212> PRT

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<223> connective tissue growth factor family motif

<221> VARIANT

<222> (2)...(9)

<223> Xaa is any amino acid

<221> VARIANT

<222> (10)...(11)

<223> Xaa is any amino acid or not present

<221> VARIANT

<222> (13)...(31)

<223> Xaa is any amino acid

<221> VARIANT

1001159-10501

<222> (32)...(32)
<223> Xaa is any amino acid or not present

<221> VARIANT
<222> (34)...(38)
<223> Xaa is any amino acid

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<222> (39)...(40)
<223> Xaa is any amino acid or not present

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<221> VARIANT
<222> (56)...(62)
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<221> VARIANT
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<223> Xaa is any amino acid

<221> VARIANT
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<223> Xaa is any amino acid or not present

<221> VARIANT
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<223> Xaa is any amino acid or not present

<400> 23
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 Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa
 20 25 30
 Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 35 40 45
 Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
 50 55 60
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 65 70 75 80
 Xaa Xaa Xaa Xaa Cys Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa
 85 90 95
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa
 100 105 110
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
 115 120 125

<210> 24

<211> 40

<212> PRT

<213> Artificial Sequence

<220>

<223> connective tissue growth factor family motif

<221> VARIANT

<222> (2)...(9)

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<222> (13)...(13)

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<222> (16)...(17)

<223> Xaa is any amino acid

<221> VARIANT

<222> (19)...(25)

<223> Xaa is any amino acid

10011359-110501

<221> VARIANT
 <222> (27)...(31)
 <223> Xaa is any amino acid

<221> VARIANT
 <222> (32)...(32)
 <223> Xaa is any amino acid or not present

<221> VARIANT
 <222> (34)...(38)
 <223> Xaa is any amino acid

<221> VARIANT
 <222> (39)...(40)
 <223> Xaa is any amino acid or not present

<400> 24

Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Cys	Cys	Xaa
1				5					10					15	
Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			20					25					30		
Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa								
			35				40								

<210> 25
 <211> 357
 <212> PRT
 <213> Homo sapiens

<400> 25

Met	Gln	Ser	Val	Gln	Ser	Thr	Ser	Phe	Cys	Leu	Arg	Lys	Gln	Cys	Leu
1				5					10					15	
Cys	Leu	Thr	Phe	Leu	Leu	Leu	His	Leu	Leu	Gly	Gln	Val	Ala	Ala	Thr
			20					25					30		
Gln	Arg	Cys	Pro	Pro	Gln	Cys	Pro	Gly	Arg	Cys	Pro	Ala	Thr	Pro	Pro
		35				40					45				
Thr	Cys	Ala	Pro	Gly	Val	Arg	Ala	Val	Leu	Asp	Gly	Cys	Ser	Cys	Cys
		50				55					60				
Leu	Val	Cys	Ala	Arg	Gln	Arg	Gly	Glu	Ser	Cys	Ser	Asp	Leu	Glu	Pro
65					70				75					80	
Cys	Asp	Glu	Ser	Ser	Gly	Leu	Tyr	Cys	Asp	Arg	Ser	Ala	Asp	Pro	Ser
			85					90					95		
Asn	Gln	Thr	Gly	Ile	Cys	Thr	Ala	Val	Glu	Gly	Asp	Asn	Cys	Val	Phe
			100					105					110		

Asp Gly Val Ile Tyr Arg Ser Gly Glu Lys Phe Gln Pro Ser Cys Lys
 115 120 125
 Phe Gln Cys Thr Cys Arg Asp Gly Gln Ile Gly Cys Val Pro Arg Cys
 130 135 140
 Gln Leu Asp Val Leu Leu Pro Glu Pro Asn Cys Pro Ala Pro Arg Lys
 145 150 155 160
 Val Glu Val Pro Gly Glu Cys Cys Glu Lys Trp Ile Cys Gly Pro Asp
 165 170 175
 Glu Glu Asp Ser Leu Gly Gly Leu Thr Leu Ala Ala Tyr Arg Pro Glu
 180 185 190
 Ala Thr Leu Gly Val Glu Val Ser Asp Ser Ser Val Asn Cys Ile Glu
 195 200 205
 Gln Thr Thr Glu Trp Thr Ala Cys Ser Lys Ser Cys Gly Met Gly Phe
 210 215 220
 Ser Thr Arg Val Thr Asn Arg Asn Arg Gln Cys Glu Met Leu Lys Gln
 225 230 235 240
 Thr Arg Leu Cys Met Val Arg Pro Cys Glu Gln Glu Pro Glu Gln Pro
 245 250 255
 Thr Asp Lys Lys Gly Lys Lys Cys Leu Arg Thr Lys Lys Ser Leu Lys
 260 265 270
 Ala Ile His Leu Gln Phe Lys Asn Cys Thr Ser Leu His Thr Tyr Lys
 275 280 285
 Pro Arg Phe Cys Gly Val Cys Ser Asp Gly Arg Cys Cys Thr Pro His
 290 295 300
 Asn Thr Lys Thr Ile Gln Ala Glu Phe Gln Cys Ser Pro Gly Gln Ile
 305 310 315 320
 Val Lys Lys Pro Val Met Val Ile Gly Thr Cys Thr Cys His Thr Asn
 325 330 335
 Cys Pro Lys Asn Asn Glu Ala Phe Leu Gln Glu Leu Glu Leu Lys Thr
 340 345 350
 Thr Arg Gly Lys Met
 355

<210> 26

<211> 349

<212> PRT

<213> Homo sapiens

<400> 26

Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe Val Val Leu
 1 5 10 15
 Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys Ser Gly Pro
 20 25 30
 Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala Gly Val Ser
 35 40 45

10011559-110601

Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu
 50 55 60
 Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu
 65 70 75 80
 Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr
 85 90 95
 Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val Tyr Arg Ser
 100 105 110
 Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp
 115 120 125
 Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val Arg Leu Pro
 130 135 140
 Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys
 145 150 155 160
 Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr Val Val Gly
 165 170 175
 Pro Ala Leu Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro
 180 185 190
 Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala
 195 200 205
 Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp
 210 215 220
 Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg
 225 230 235 240
 Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys
 245 250 255
 Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu Ser Gly
 260 265 270
 Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr
 275 280 285
 Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro Val Glu
 290 295 300
 Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met Met Phe Ile
 305 310 315 320
 Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe
 325 330 335
 Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala
 340 345

<210> 27

<211> 259

<212> PRT

<213> Homo sapiens

<400> 27

Met Ser Glu Val Pro Val Ala Arg Val Trp Leu Val Leu Leu Leu Leu
 1 5 10 15
 Thr Val Gln Val Gly Val Thr Ala Gly Ala Pro Trp Gln Cys Ala Pro
 20 25 30
 Cys Ser Ala Glu Lys Leu Ala Leu Cys Pro Pro Val Ser Ala Ser Cys
 35 40 45
 Ser Glu Val Thr Arg Ser Ala Gly Cys Gly Cys Cys Pro Met Cys Ala
 50 55 60
 Leu Pro Leu Gly Ala Ala Cys Gly Val Ala Thr Ala Arg Cys Ala Arg
 65 70 75 80
 Gly Leu Ser Cys Arg Ala Leu Pro Gly Glu Gln Gln Pro Leu His Ala
 85 90 95
 Leu Thr Arg Gly Gln Gly Ala Cys Val Gln Glu Ser Asp Ala Ser Ala
 100 105 110
 Pro His Ala Ala Glu Ala Gly Ser Pro Glu Ser Pro Glu Ser Thr Glu
 115 120 125
 Ile Thr Glu Glu Glu Leu Leu Asp Asn Phe His Leu Met Ala Pro Ser
 130 135 140
 Glu Glu Asp His Ser Ile Leu Trp Asp Ala Ile Ser Thr Tyr Asp Gly
 145 150 155 160
 Ser Lys Ala Leu His Val Thr Asn Ile Lys Lys Trp Lys Glu Pro Cys
 165 170 175
 Arg Ile Glu Leu Tyr Arg Val Val Glu Ser Leu Ala Lys Ala Gln Glu
 180 185 190
 Thr Ser Gly Glu Glu Ile Ser Lys Phe Tyr Leu Pro Asn Cys Asn Lys
 195 200 205
 Asn Gly Phe Tyr His Ser Arg Gln Cys Glu Thr Ser Met Asp Gly Glu
 210 215 220
 Ala Gly Leu Cys Trp Cys Val Tyr Pro Trp Asn Gly Lys Arg Ile Pro
 225 230 235 240
 Gly Ser Pro Glu Ile Arg Gly Asp Pro Asn Cys Gln Ile Tyr Phe Asn
 245 250 255
 Val Gln Asn

<210> 28

<211> 328

<212> PRT

<213> Homo sapiens

<400> 28

Met Leu Pro Arg Val Gly Cys Pro Ala Leu Pro Leu Pro Pro Pro Pro
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 20 25 30

Gly Gly Gly Gly Ala Arg Ala Glu Val Leu Phe Arg Cys Pro Pro Cys
 35 40 45
 Thr Pro Glu Arg Leu Ala Ala Cys Gly Pro Pro Pro Val Ala Pro Pro
 50 55 60
 Ala Ala Val Ala Ala Val Ala Gly Gly Ala Arg Met Pro Cys Ala Glu
 65 70 75 80
 Leu Val Arg Glu Pro Gly Cys Gly Cys Cys Ser Val Cys Ala Arg Leu
 85 90 95
 Glu Gly Glu Ala Cys Gly Val Tyr Thr Pro Arg Cys Gly Gln Gly Leu
 100 105 110
 Arg Cys Tyr Pro His Pro Gly Ser Glu Leu Pro Leu Gln Ala Leu Val
 115 120 125
 Met Gly Glu Gly Thr Cys Glu Lys Arg Arg Asp Ala Glu Tyr Gly Ala
 130 135 140
 Ser Pro Glu Gln Val Ala Asp Asn Gly Asp Asp His Ser Glu Gly Gly
 145 150 155 160
 Leu Val Glu Asn His Val Asp Ser Thr Met Asn Met Leu Gly Gly Gly
 165 170 175
 Gly Ser Ala Gly Arg Lys Pro Leu Lys Ser Gly Met Lys Glu Leu Ala
 180 185 190
 Val Phe Arg Glu Lys Val Thr Glu Gln His Arg Gln Met Gly Lys Gly
 195 200 205
 Gly Lys His His Leu Gly Leu Glu Glu Pro Lys Lys Leu Arg Pro Pro
 210 215 220
 Pro Ala Arg Thr Pro Cys Gln Gln Glu Leu Asp Gln Val Leu Glu Arg
 225 230 235 240
 Ile Ser Thr Met Arg Leu Pro Asp Glu Arg Gly Pro Leu Glu His Leu
 245 250 255
 Tyr Ser Leu His Ile Pro Asn Cys Asp Lys His Gly Leu Tyr Asn Leu
 260 265 270
 Lys Gln Cys Lys Met Ser Leu Asn Gly Gln Arg Gly Glu Cys Trp Cys
 275 280 285
 Val Asn Pro Asn Thr Gly Lys Leu Ile Gln Gly Ala Pro Thr Ile Arg
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